

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: THE BOARD OF TRUSTEES OF THE LELAND STANFORD JUNIOR UNIVERSITY

(ii) TITLE OF INVENTION: Patched Genes and their Use

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
- (B) STREET: Four Embarcadero Center, Suite 3400
- (C) CITY: San Francisco
- (D) STATE: CA
- (E) COUNTRY: US
- (F) ZIP: 94111

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US95/
- (B) FILING DATE: 06-OCT-1995
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Rowland, Bertram I
- (B) REGISTRATION NUMBER: 20015
- (C) REFERENCE/DOCKET NUMBER: a60190-1

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 415-781-1989
- (B) TELEFAX: 415-398-3249

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AACNNC NNTN NATGGCACCC CCNCCCAACC TTTNNNCCNN NTAANCAAAA NNCCCCNTTT

60

NATACCCCT NTAAANT TCCACCNNNC NNAAANNCCN CTGNANAC NGNAAANCCN 120
 TTTTNAACC CCCCCACCC GGAATTCNA NTNCCNCCC CCAAATTACA ACTCCAGNCC 180
 AAAATTNANA NAATTGGTCC TAACCTAACC NATNGTTGTT ACGGTTTCCC CCCCCAAATA 240
 CATGCACTGG CCCGAACACT TGATCGTTGC CGTTCCAATA AGAATAAATC TGGTCATATT 300
 AAACAAGCCN AAAGCTTTAC AACTGTTGT ACAATTAATG GGCGAACACG AACTGTTTGA 360
 ATTCTGGTCT GGACATTACA AAGTGCACCA CATCGGATGG AACCAGGAGA AGGCCACAAC 420
 CGTACTGAAC GCCTGGCAGA AGAAGTTCGC ACAGGTTGGT GGTGGCGCA AGGAGTAGAG 480
 TGAATGGTGG TAATTTTTGG TTGTTCCAGG AGGTGGATCG TCTGACGAAG AGCAAGAAGT 540
 CGTCGAATTA CATCTTCGTG ACGTTCTCCA CCGCCAATTT GAACAAGATG TTGAAGGAGG 600
 CGTCGAANAC GGACGTGGTG AAGCTGGGGG TGGTGCTGGG GGTGGCGGCG GTGTACGGGT 660
 GGGTGGCCCA GTCGGGGCTG GCTGCCTTGG GAGTGCTGGT CTTNGCGNGC TNCNATTCGC 720
 CCTATAGTNA GNCGTA 736

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa	Pro	Pro	Pro	Asn	Tyr	Asn	Ser	Xaa	Pro	Lys	Xaa	Xaa	Xaa	Leu	Val
1				5					10					15	
Leu	Thr	Pro	Xaa	Val	Val	Thr	Val	Ser	Pro	Pro	Lys	Tyr	Met	His	Trp
			20					25					30		
Pro	Glu	His	Leu	Ile	Val	Ala	Val	Pro	Ile	Arg	Ile	Asn	Leu	Val	Ile
		35					40					45			
Leu	Asn	Lys	Pro	Lys	Ala	Leu	Gln	Thr	Val	Val	Gln	Leu	Met	Gly	Glu
	50					55					60				
His	Glu	Leu	Phe	Glu	Phe	Trp	Ser	Gly	His	Tyr	Lys	Val	His	His	Ile
65				70					75						80
Gly	Trp	Asn	Gln	Glu	Lys	Ala	Thr	Thr	Val	Leu	Asn	Ala	Trp	Gln	Lys
			85						90					95	
Lys	Phe	Ala	Gln	Val	Gly	Gly	Trp	Arg	Lys	Glu					

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGTCTGTCA CCCGGAGCCG GAGTCCCCGG CGGCCAGCAG CGTCCTCGCG AGCCGAGCGC 60
CCAGGCGCGC CCGGAGCCCC CGGCGGCGGC GGCAACATGG CCTCGGCTGG TAACGCCGCC 120
GGGGCCCTGG GCAGGCAGGC CGGCGGCGGG AGGCGCAGAC GGACCGGGGG ACCGCACCGC 180
GCCGCGCCGG ACCGGGACTA TCTGCACCGG CCCAGCTACT GCGACGCCGC CTTCGCTCTG 240
GAGCAGATTT CCAAGGGGAA GGCTACTGGC CGGAAAGCGC CGCTGTGGCT GAGAGCGAAG 300
TTTCAGAGAC TCTTATTTAA ACTGGGTTGT TACATTCAA AGAACTGCGG CAAGTTTTTG 360
GTTGTGGGTC TCCTCATATT TGGGGCCTTC GCTGTGGGAT TAAAGGCAGC TAATCTCGAG 420
ACCAACGTGG AGGAGCTGTG GGTGGAAGTT GGTGGACGAG TGAGTCGAGA ATTAAATTAT 480
ACCCGTCAGA AGATAGGAGA AGAGGCTATG TTTAATCCTC AACTCATGAT ACAGACTCCA 540
AAAGAAGAAG GCGCTAATGT TCTGACCACA GAGGCTCTCC TGCAACACCT GGA CTCAGCA 600
CTCCAGGCCA GTCGTGTGCA CGTCTACATG TATAACAGGC AATGGAAGTT GGAACATTG 660
TGCTACAAAT CAGGGGAACT TATCACGGAG ACAGGTTACA TGGATCAGAT AATAGAATAC 720
CTTTACCCTT GCTTAATCAT TACACCTTTG GACTGCTTCT GGGAAGGGGC AAAGCTACAG 780
TCCGGGACAG CATACTCCT AGGTAAGCCT CCTTTACGGT GGACAACTT TGACCCCTTG 840
GAATTCCTAG AAGAGTTAAA GAAAATAAAC TACCAAGTGG ACAGCTGGGA GGAAATGCTG 900
AATAAGCCG AAGTTGGCCA TGGGTACATG GACCGGCCTT GCCTCAACCC AGCCGACCCA 960
GATTGCCCTG CCACAGCCCC TAACAAAAT TCAACCAAAC CTCTTGATGT GGCCCTTGTT 1020
TTGAATGGTG GATGTCAAGG TTTATCCAGG AAGTATATGC ATTGGCAGGA GGAGTTGATT 1080
GTGGGTGGTA CCGTCAAGAA TGCCACTGGA AAAGTTGTCA GCGCTCACGC CCTGCAAACC 1140
ATGTTCCAGT TAATGACTCC CAAGCAAATG TATGAACACT TCAGGGGCTA CGACTATGTC 1200
TCTCACATCA ACTGGAATGA AGACAGGGCA GCCGCCATCC TGGAGGCCTG GCAGAGGACT 1260

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TACGTGGAGG TGGTTCA	AAGTGTGCGC CCAAACCTCCA CTCAAAA	GCTTCCCTTC	1320
ACAACCACGA CCCTGGACGA CATCCTAAAA TCCTTCTCTG ATGTCAGTGT CATCCGAGTG			1380
GCCAGCGGCT ACCTACTGAT GCTTGCCTAT GCCTGTTTAA CCATGCTGCG CTGGGACTGC			1440
TCCAAGTCCC AGGGTGCCGT GGGGCTGGCT GCGCTCCTGT TGGTTGCGCT GTCAGTGGCT			1500
GCAGGATTGG GCCTCTGCTC CTTGATTGGC ATTTCTTTTA ATGCTGCGAC AACTCAGGTT			1560
TTGCCGTTTC TTGCTCTTGG TGTGGGTGTG GATGATGTCT TCCTCCTGGC CCATGCATTC			1620
AGTGAAACAG GACAGAATAA GAGGATTCCA TTTGAGGACA GGAAGTGGGA GTGCCTCAAG			1680
CGCACCAGGAG CCAGCGTGGC CCTCACCTCC ATCAGCAATG TCACCGCCTT CTTTCATGGCC			1740
GCATTGATCC CTATCCCTGC CCTGCGAGCG TTCTCCCTCC AGGCTGCTGT GGTGGTGGTA			1800
TTCAATTTTG CTATGGTTCT GCTCATTITT CCTGCAATTC TCAGCATGGA TTTATACAGA			1860
CGTGAGGACA GAAGATTGGA TATTTTCTGC TGTTCACAA GCCCCTGTGT CAGCAGGGTG			1920
ATTCAAGTTG AGCCACAGGC CTACACAGAG CCTCACAGTA ACACCCGGTA CAGCCCCCA			1980
CCCCCATACA CCAGCCACAG CTTGCCCCAC GAAACCCATA TCACTATGCA GTCCACCGTT			2040
CAGCTCCGCA CAGAGTATGA CCCTCACACG CACGTGTACT ACACCACCGC CGAGCCACGC			2100
TCTGAGATCT CTGTACAGCC TGTACCGTC ACCCAGGACA ACCTCAGCTG TCAGAGTCCC			2160
GAGAGCACCA GCTCTACCAG GGACCTGCTC TCCCAGTTCT CAGACTCCAG CCTCCACTGC			2220
CTCGAGCCCC CCTGCACCAA GTGGACACTC TCTTCGTTTG CAGAGAAGCA CTATGCTCCT			2280
TTCTCCTGA AACCCAAAGC CAAGGTTGTG GTAATCCTTC TTTTCTGGG CTTGCTGGGG			2340
GTCAGCCTTT ATGGGACCAC CCGAGTGAGA GACGGGCTGG ACCTCACGGA CATTGTTCCC			2400
CGGGAAACCA GAGAATATGA CTTCATAGCT GCCCAGTTCA AGTACTTCTC TTTCTACAAC			2460
ATGTATATAG TCACCCAGAA AGCAGACTAC CCGAATATCC AGCACCTACT TTACGACCTT			2520
CATAAGAGTT TCAGCAATGT GAAGTATGTC ATGCTGGAGG AGAACAAGCA ACTTCCCCAA			2580
ATGTGGCTGC ACTACTTTAG AGACTGGCTT CAAGGACTTC AGGATGCATT TGACAGTGAC			2640
TGGGAAACTG GGAGGATCAT GCCAAACAAT TATAAAAATG GATCAGATGA CGGGGTCCTC			2700
GCTTACAAAC TCCTGGTGCA GACTGGCAGC CGAGACAAGC CCATCGACAT TAGTCAGTTG			2760
ACTAAACAGC GTCTGGTAGA CGCAGATGGC ATCATTAAATC CGAGCGCTTT CTACATCTAC			2820
CTGACCGCTT GGGTCAGCAA CGACCCTGTA GCTTACGCTG CCTCCCAGGC CAACATCCGG			2880
CCTCACCGGC CGGAGTGGGT CCATGACAAA GCCGACTACA TGCCAGAGAC CAGGCTGAGA			2940
ATCCCAGCAG CAGAGCCCAT CGAGTACGCT CAGTTCCCTT TCTACCTCAA CGGCCTACGA			3000

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GACACCTCAG ACTTTGTG AGCCATAGAA AAAGTGAGAG TCATCTG CAACTATACG	3060
AGCCTGGGAC TGTCCAGCTA CCCCAATGGC TACCCCTTCC TGTTCCTGGGA GCAATACATC	3120
AGCCTGCGCC ACTGGCTGCT GCTATCCATC AGCGTGGTGC TGGCCTGCAC GTTTCTAGTG	3180
TGCGCAGTCT TCCTCCTGAA CCCCTGGACG GCCGGGATCA TTGTCATGGT CCTGGCTCTG	3240
ATGACCGTTG AGCTCTTTGG CATGATGGGC CTCATTGGGA TCAAGCTGAG TGCTGTGCCT	3300
GTGGTCATCC TGATTGCATC TGTGGGCATC GGAGTGGAGT TCACCGTCCA CGTGGCTTTG	3360
GCCTTTCTGA CAGCCATTGG GGACAAGAAC CACAGGGCTA TGCTCGCTCT GGAACACATG	3420
TTTGCTCCCG TTCTGGACGG TGCTGTGTCC ACTCTGCTGG GTGTACTGAT GCTTGCAGGG	3480
TCCGAATTTG ATTTCAATTGT CAGATACTTC TTTGCCGTCC TGGCCATTCT CACCGTCTTG	3540
GGGGTTCTCA ATGGACTGGT TCTGCTGCCT GTCCTCTTAT CCTTCTTTGG ACCGTGTCCT	3600
GAGGTGTCTC CAGCCAATGG CCTAAACCGA CTGCCCCTC CTTCGCCTGA GCCGCCTCCA	3660
AGTGTCTGCC GGTTCGCCGT GCCTCCTGGT CACACGAACA ATGGGTCTGA TTCCTCCGAC	3720
TCGGAGTACA GCTCTCAGAC CACGGTGTCT GGCATCAGTG AGGAGCTCAG GCAATACGAA	3780
GCACAGCAGG GTGCCGGAGG CCCTGCCCAC CAAGTGATTG TGGAAGCCAC AGAAAACCCT	3840
GTCTTTGCCC GGTCCACTGT GGTCCATCCG GACTCCAGAC ATCAGCCTCC CTTGACCCCT	3900
CGGCAACAGC CCCACCTGGA CTCTGGCTCC TTGTCCCCTG GACGGCAAGG CCAGCAGCCT	3960
CGAAGGGATC CCCCTAGAGA AGGCTTGCGG CCACCCCCCT ACAGACCGCG CAGAGACGCT	4020
TTTGAAATTT CTAAGAAGG GCATTCTGGC CCTAGCAATA GGGACCGCTC AGGGCCCCGT	4080
GGGGCCCGTT CTCACAACCC TCGGAACCCA ACGTCCACCG CCATGGGCAG CTCTGTGCCC	4140
AGCTACTGCC AGCCCATCAC CACTGTGACG GCTTCTGCTT CGGTGACTGT TGCTGTGCAT	4200
CCCCCGCCTG GACCTGGGCG CAACCCCCGA GGGGGGCCCT GTCCAGGCTA TGAGAGCTAC	4260
CCTGAGACTG ATCACGGGGT ATTTGAGGAT CCTCATGTGC CTTTTCATGT CAGGTGTGAG	4320
AGGAGGGACT CAAAGGTGGA GGTCATAGAG CTACAGGACG TGGAATGTGA GGAGAGGCCG	4380
TGGGGGAGCA GCTCCAACCTG AGGGTAATTA AAATCTGAAG CAAAGAGGCC AAAGATTGGA	4440
AAGCCCCGCC CCCACCTCTT TCCAGAACTG CTTGAAGAGA ACTGCTTGGA ATTATGGGAA	4500
GGCAGTTCAT TGTTACTGTA ACTGATTGTA TTATTKKGTG AAATATTTCT ATAAATATTT	4560
AARAGGTGTA CACATGTAAT ATACATGGAA ATGCTGTACA GTCTATTTCC TGGGGCCTCT	4620
CCACTCCTGC CCCAGAGTGG GGAGACCACA GGGGCCCTTT CCCCTGTGTA CATTGGTCTC	4680
TGTGCCACAA CCAAGCTTAA CTTAGTTTTA AAAAAATCT CCCAGCATAT GTCGCTGCTG	4740

CTTAAATATT GTATAATT CTGTGTATAAT TCTATGCAAA TATTGCTT TAATAGGAT 4800
TATTTGTAAA GGTTCCTGTT TAAAATATTT TAAATTTGCA TATCACAACC CTGTGGTAGG 4860
ATGAATTGTT ACTGTAACT TTTGAACACG CTATGCGTGG TAATTGTTTA ACGAGCAGAC 4920
ATGAAGAAAA CAGGTTAATC CCAGTGGCTT CTCTAGGGGT AGTTGTATAT GGTTCGCATG 4980
GGTGGATGTG TGTGTGCATG TGACTTTCCA ATGTACTGTA TTGTGGTTTG TTGTTGTTGT 5040
TGCTGTTGTT GTTCATTTTG GTGTTTTTGG TTGCTTTGTA TGATCTTAGC TCTGGCCTAG 5100
GTGGGCTGGG AAGGTCCAGG TCTTTTCTG TCGTGATGCT GGTGGAAAGG TGACCCCAAT 5160
CATCTGTCCT ATTCTCTGGG ACTATTC 5187

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Val	Ala	Pro	Asp	Ser	Glu	Ala	Pro	Ser	Asn	Pro	Arg	Ile	Thr	Ala	1	5	10	15
Ala	His	Glu	Ser	Pro	Cys	Ala	Thr	Glu	Ala	Arg	His	Ser	Ala	Asp	Leu	20	25	30	
Tyr	Ile	Arg	Thr	Ser	Trp	Val	Asp	Ala	Ala	Leu	Ala	Leu	Ser	Glu	Leu	35	40	45	
Glu	Lys	Gly	Asn	Ile	Glu	Gly	Gly	Arg	Thr	Ser	Leu	Trp	Ile	Arg	Ala	50	55	60	
Trp	Leu	Gln	Glu	Gln	Leu	Phe	Ile	Leu	Gly	Cys	Phe	Leu	Gln	Gly	Asp	65	70	75	80
Ala	Gly	Lys	Val	Leu	Phe	Val	Ala	Ile	Leu	Val	Leu	Ser	Thr	Phe	Cys	85	90	95	
Val	Gly	Leu	Lys	Ser	Ala	Gln	Ile	His	Thr	Arg	Val	Asp	Gln	Leu	Trp	100	105	110	
Val	Gln	Glu	Gly	Gly	Arg	Leu	Glu	Ala	Glu	Leu	Lys	Tyr	Thr	Ala	Gln	115	120	125	
Ala	Leu	Gly	Glu	Ala	Asp	Ser	Thr	His	Gln	Leu	Val	Ile	Gln	Thr		130	135	140	

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Ala Lys Asp Pasp Val Ser Leu Leu His Pro Gl a Leu Leu Glu
145 150 155 160

His Leu Lys Val Val His Ala Ala Thr Arg Val Thr Val His Met Tyr
165 170 175

Asp Ile Glu Trp Arg Leu Lys Asp Leu Cys Tyr Ser Pro Ser Ile Pro
180 185 190

Asp Phe Glu Gly Tyr His His Ile Glu Ser Ile Ile Asp Asn Val Ile
195 200 205

Pro Cys Ala Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly Ser Lys
210 215 220

Leu Leu Gly Pro Asp Tyr Pro Ile Tyr Val Pro His Leu Lys His Lys
225 230 235 240

Leu Gln Trp Thr His Leu Asn Pro Leu Glu Val Val Glu Glu Val Lys
245 250 255

Lys Leu Lys Phe Gln Phe Pro Leu Ser Thr Ile Glu Ala Tyr Met Lys
260 265 270

Arg Ala Gly Ile Thr Ser Ala Tyr Met Lys Lys Pro Cys Leu Asp Pro
275 280 285

Thr Asp Pro His Cys Pro Ala Thr Ala Pro Asn Lys Lys Ser Gly His
290 295 300

Ile Pro Asp Val Ala Ala Glu Leu Ser His Gly Cys Tyr Gly Phe Ala
305 310 315 320

Ala Ala Tyr Met His Trp Pro Glu Gln Leu Ile Val Gly Gly Ala Thr
325 330 335

Arg Asn Ser Thr Ser Ala Leu Arg Lys Ala Arg Xaa Leu Gln Thr Val
340 345 350

Val Gln Leu Met Gly Glu Arg Glu Met Tyr Glu Tyr Trp Ala Asp His
355 360 365

Tyr Lys Val His Gln Ile Gly Trp Asn Gln Glu Lys Ala Ala Ala Val
370 375 380

Leu Asp Ala Trp Gln Arg Lys Phe Ala Ala Glu Val Arg Lys Ile Thr
385 390 395 400

Thr Ser Gly Ser Val Ser Ser Ala Tyr Ser Phe Tyr Pro Phe Ser Thr
405 410 415

Ser Thr Leu Asn Asp Ile Leu Gly Lys Phe Ser Glu Val Ser Leu Lys
420 425 430

Asn Ile Ile Leu Gly Tyr Met Phe Met Leu Ile Tyr Val Ala Val Thr
435 440 445

Leu Ile Gln Trp Arg Asp Pro Il Arg Ser Gln Ala Gly Val Gly Ile

Ala Gly Val Leu Leu Leu Ser Ile Thr Val Ala Ala Gly Leu Gly Phe
465 470 475 480

Cys Ala Leu Leu Gly Ile Pro Phe Asn Ala Ser Ser Thr Gln Ile Val
485 490 495

Pro Phe Leu Ala Leu Gly Leu Gly Val Gln Asp Met Phe Leu Leu Thr
500 505 510

His Thr Tyr Val Glu Gln Ala Gly Asp Val Pro Arg Glu Glu Arg Thr
515 520 525

Gly Leu Val Leu Lys Lys Ser Gly Leu Ser Val Leu Leu Ala Ser Leu
530 535 540

Cys Asn Val Met Ala Phe Leu Ala Ala Ala Leu Leu Pro Ile Pro Ala
545 550 555 560

Phe Arg Val Phe Cys Leu Gln Ala Ala Ile Leu Leu Leu Phe Asn Leu
565 570 575

Gly Ser Ile Leu Leu Val Phe Pro Ala Met Ile Ser Leu Asp Leu Arg
580 585 590

Arg Arg Ser Ala Ala Arg Ala Asp Leu Leu Cys Cys Leu Met Pro Glu
595 600 605

Ser Pro Leu Pro Lys Lys Lys Ile Pro Glu Arg Ala Lys Thr Arg Lys
610 615 620

Asn Asp Lys Thr His Arg Ile Asp Thr Thr Arg Gln Pro Leu Asp Pro
625 630 635 640

Asp Val Ser Glu Asn Val Thr Lys Thr Cys Cys Leu Ser Val Ser Leu
645 650 655

Thr Lys Trp Ala Lys Asn Gln Tyr Ala Pro Phe Ile Met Arg Pro Ala
660 665 670

Val Lys Val Thr Ser Met Leu Ala Leu Ile Ala Val Ile Leu Thr Ser
675 680 685

Val Trp Gly Ala Thr Lys Val Lys Asp Gly Leu Asp Leu Thr Asp Ile
690 695 700

Val Pro Glu Asn Thr Asp Glu His Glu Phe Leu Ser Arg Gln Glu Lys
705 710 715 720

Tyr Phe Gly Phe Tyr Asn Met Tyr Ala Val Thr Gln Gly Asn Phe Glu
725 730 735

Tyr Pro Thr Asn Gln Lys Leu Leu Tyr Glu Tyr His Asp Gln Phe Val
740 745 750

Arg Ile Pro Asn Ile Ile Lys Asn Asp Asn Gly Gly Leu Thr Lys Phe
755 760 765

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Trp Leu Ser Phe Arg Asp Trp Leu Leu Asp Leu Val Ala Phe
770 775 780

Asp Lys Glu Val Ala Ser Gly Cys Ile Thr Gln Glu Tyr Trp Cys Lys
785 790 795 800

Asn Ala Ser Asp Glu Gly Ile Leu Ala Tyr Lys Leu Met Val Gln Thr
805 810 815

Gly His Val Asp Asn Pro Ile Asp Lys Ser Leu Ile Thr Ala Gly His
820 825 830

Arg Leu Val Asp Lys Asp Gly Ile Ile Asn Pro Lys Ala Phe Tyr Asn
835 840 845

Tyr Leu Ser Ala Trp Ala Thr Asn Asp Ala Leu Ala Tyr Gly Ala Ser
850 855 860

Gln Gly Asn Leu Lys Pro Gln Pro Gln Arg Trp Ile His Ser Pro Glu
865 870 875 880

Asp Val His Leu Glu Ile Lys Lys Ser Ser Pro Leu Ile Tyr Thr Gln
885 890 895

Leu Pro Phe Tyr Leu Ser Gly Leu Ser Asp Thr Xaa Ser Ile Lys Thr
900 905 910

Leu Ile Arg Ser Val Arg Asp Leu Cys Leu Lys Tyr Glu Ala Lys Gly
915 920 925

Leu Pro Asn Phe Pro Ser Gly Ile Pro Phe Leu Phe Trp Glu Gln Tyr
930 935 940

Leu Tyr Leu Arg Thr Ser Leu Leu Leu Ala Leu Ala Cys Ala Leu Ala
945 950 955 960

Ala Val Phe Ile Ala Val Met Val Leu Leu Leu Asn Ala Trp Ala Ala
965 970 975

Val Leu Val Thr Leu Ala Leu Ala Thr Leu Val Leu Gln Leu Leu Gly
980 985 990

Val Met Ala Leu Leu Gly Val Lys Leu Ser Ala Met Pro Ala Val Leu
995 1000 1005

Leu Val Leu Ala Ile Gly Arg Gly Val His Phe Thr Val His Leu Cys
1010 1015 1020

Leu Gly Phe Val Thr Ser Ile Gly Cys Lys Arg Arg Arg Ala Ser Leu
1025 1030 1035 1040

Ala Leu Glu Ser Val Leu Ala Pro Val Val His Gly Ala Leu Ala Ala
1045 1050 1055

Ala Leu Ala Ala Ser Met Leu Ala Ala Ser Glu Cys Gly Phe Val Ala
1060 1065 1070

Arg Leu Phe Leu Arg Leu Leu Leu Asp Ile Val Phe Leu Gly Leu Ile

Asp Gly Leu Leu Phe Phe Pro Ile Val Leu Ser Ile Leu Gly Pro Ala
 1090 1095 1100

Ala Glu Val Arg Pro Ile Glu His Pr Glu Arg Leu Ser Thr Pro Ser
 1105 1110 1115 1120

Pro Lys Cys Ser Pr Ile His Pro Arg Lys Ser Ser Ser Ser Gly
 1125 1130 1135

Gly Gly Asp Lys Ser Ser Arg Thr Ser Lys Ser Ala Pro Arg Pro Cys
 1140 1145 1150

Ala Pro Ser Leu Thr Thr Ile Thr Glu Glu Pro Ser Ser Trp His Ser
 1155 1160 1165

Ser Ala His Ser Val Gln Ser Ser Met Gln Ser Ile Val Val Gln Pro
 1170 1175 1180

Glu Val Val Val Glu Thr Thr Thr Tyr Asn Gly Ser Asp Ser Ala Ser
 1185 1190 1195 1200

Gly Arg Ser Thr Pro Thr Lys Ser Ser His Gly Gly Ala Ile Thr Thr
 1205 1210 1215

Thr Lys Val Thr Ala Thr Ala Asn Ile Lys Val Glu Val Val Thr Pro
 1220 1225 1230

Ser Asp Arg Lys Ser Arg Arg Ser Tyr His Tyr Tyr Asp Arg Arg Arg
 1235 1240 1245

Asp Arg Asp Glu Asp Arg Asp Arg Asp Arg Glu Arg Asp Arg Asp Arg
 1250 1255 1260

Asp Arg Asp Arg Asp Arg Asp Arg Asp Arg Asp Arg Asp Arg
 1265 1270 1275 1280

Glu Arg Ser Arg Glu Arg Asp Arg Arg Asp Arg Tyr Arg Asp Glu Arg
 1285 1290 1295

Asp His Arg Ala Ser Pro Arg Glu Lys Arg Gln Arg Phe Trp Thr
 1300 1305 1310

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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CGAAACAAGA	GAGCGAGTGA	TAGGGAG	AGCGTCTGTG	TTGTGTGTTG	GTGCGCC	60
ACGCACACAG	GCGCAAAACA	GTGCACACAG	ACGCCCCGCTG	GGCAAGAGAG	AGTGAGAGAG	120
AGAAACAGCG	GCGCGCGCTC	GCCTAATGAA	GTTGTTGGCC	TGGCTGGCGT	GCCGCATCCA	180
CGAGATACAG	ATACATCTCT	CATGGACCGC	GACAGCCTCC	CACGCGTTCC	GGACACACAC	240
GGCGATGTGG	TCGATGAGAA	ATTATTCTCG	GATCTTTACA	TACGCACCAG	CTGGGTGGAC	300
GCCCAAGTGG	CGCTCGATCA	GATAGATAAG	GGCAAAGCGC	GTGGCAGCCG	CACGGCGATC	360
TATCTGCGAT	CAGTATTCCA	GTCCCACCTC	GAAACCCTCG	GCAGCTCCGT	GCAAAAGCAC	420
GCGGGCAAGG	TGCTATTCTG	GGCTATCCTG	GTGCTGAGCA	CCTTCTGCGT	CGGCCTGAAG	480
AGCGCCCAGA	TCCACTCCAA	GGTGCACCAG	CTGTGGATCC	AGGAGGGCGG	CCGGCTGGAG	540
GCGGAACTGG	CCTACACACA	GAAGACGATC	GGCGAGGACG	AGTCGGCCAC	GCATCAGCTG	600
CTCATTGAGA	CGACCCACGA	CCCGAACGCC	TCCGTCCTGC	ATCCGCAGGC	GCTGCTTGCC	660
CACCTGGAGG	TCCTGGTCAA	GGCCACCGCC	GTCAAGGTGC	ACCTCTACGA	CACCGAATGG	720
GGGCTGCGCG	ACATGTGCAA	CATGCCGAGC	ACGCCCTCCT	TCGAGGGCAT	CTACTACATC	780
GAGCAGATCC	TGCGCCACCT	CATTCCGTGC	TCGATCATCA	CGCCGCTGGA	CTGTTTCTGG	840
GAGGGAAGCC	AGCTGTTGGG	TCCGGAATCA	GCGGTCGTTA	TACCAGGCCT	CAACCAACGA	900
CTCCTGTGGA	CCACCCTGAA	TCCCGCCTCT	GTGATGCAGT	ATATGAAACA	AAAGATGTCC	960
GAGGAAAAGA	TCAGCTTCGA	CTTCGAGACC	GTGGAGCAGT	ACATGAAGCG	TGCGGCCATT	1020
GGCAGTGGCT	ACATGGAGAA	GCCCTGCCTG	AACCCACTGA	ATCCCAATTG	CCCGGACACG	1080
GCACCGAACA	AGAACAGCAC	CCAGCCGCCG	GATGTGGGAG	CCATCCTGTC	CGGAGGCTGC	1140
TACGGTTATG	CCGCGAAGCA	CATGCACTGG	CCGGAGGAGC	TGATTGTGGG	CGGACGGAAG	1200
AGGAACCGCA	GCGGACACTT	GAGGAAGGCC	CAGGCCCTGC	AGTCGGTGGT	GCAGCTGATG	1260
ACCGAGAAGG	AAATGTACGA	CCAGTGGCAG	GACAACTACA	AGGTGCACCA	TCTTGGATGG	1320
ACGCAGGAGA	AGGCAGCGGA	GGTTTTGAAC	GCCTGGCAGC	GCAACTTTTC	GCGGGAGGTG	1380
GAACAGCTGC	TACGTAAACA	GTCGAGAATT	GCCACCAACT	ACGATATCTA	CGTGTTTCAGC	1440
TCGGCTGCAC	TGGATGACAT	CCTGGCCAAG	TTCTCCCATC	CCAGCGCCTT	GTCCATTGTC	1500
ATCGGCGTGG	CCGTCACCGT	TTTGTATGCC	TTTGCACGC	TCCTCCGCTG	GAGGGACCCC	1560
GTCCGTGGCC	AGAGCAGTGT	GGGCGTGGCC	GGAGTTCTGC	TCATGTGCTT	CAGTACCGCC	1620
GCCGGATTGG	GATTGTCAGC	CCTGCTCGGT	ATCGTTTTCA	ATGCGCTGAC	CGCTGCCTAT	1680
GCGGAGAGCA	ATCGGCGGGA	GCAGACCAAG	CTGATTCTCA	AGAACGCCAG	CACCCAGGTG	1740

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GTTCCGTTTT	TGGCCCT	TCTGGGCGTC	GATCACATCT	TCATAGT	ACCGAGCATC	1800
CTGTTCACTG	CCTGCAGCAC	CGCAGGATCC	TTCTTTGCGG	CCGCCTTTAT	TCCGGTGCCG	1860
GCTTTGAAGG	TATTCTGTCT	GCAGGCTGCC	ATCGTAATGT	GCTCCAATTT	GGCAGCGGCT	1920
CTATTGGTTT	TTCGGCCAT	GATTTCTGTTG	GATCTACGGA	GACGTACCGC	CGGCAGGGCG	1980
GACATCTTCT	GCTGCTGTTT	TCCGGTGTGG	AAGGAACAGC	CGAAGGTGGC	ACCTCCGGTG	2040
CTGCCGCTGA	ACAACAACAA	CGGGCGCGGG	GCCCGGCATC	CGAAGAGCTG	CAACAACAAC	2100
AGGGTGCCGC	TGCCCCCCA	GAATCCTCTG	CTGGAACAGA	GGGCAGACAT	CCCTGGGAGC	2160
AGTCACTCAC	TGGCGTCCTT	CTCCCTGGCA	ACCTTCGCCT	TTCAGCACTA	CACTCCCTTC	2220
CTCATGCGCA	GCTGGGTGAA	GTTCTTGACC	GTTATGGGTT	TCCTGGCGGC	CCTCATATCC	2280
AGCTTGATG	CCTCCACGCG	CCTTCAGGAT	GGCCTGGACA	TTATTGATCT	GGTGCCCAAG	2340
GACAGCAACG	AGCACAAGTT	CCTGGATGCT	CAAACCTCGC	TCTTTGGCTT	CTACAGCATG	2400
TATGCGGTTA	CCCAGGGCAA	CTTTGAATAT	CCCACCCAGC	AGCAGTTGCT	CAGGGACTAC	2460
CATGATTCCT	TTGTGCGGGT	GCCACATGTG	ATCAAGAATG	ATAACGGTGG	ACTGCCGGAC	2520
TTCTGGCTGC	TGCTCTTCAG	CGAGTGGCTG	GGTAATCTGC	AAAAGATATT	CGACGAGGAA	2580
TACCGCGACG	GACGGCTGAC	CAAGGAGTGC	TGGTTCCCAA	ACGCCAGCAG	CGATGCCATC	2640
CTGGCCTACA	AGCTAATCGT	GCAAACCGGC	CATGTGGACA	ACCCCGTGGA	CAAGGAACTG	2700
GTGCTACCA	ATCGCCTGGT	CAACAGCGAT	GGCATCATCA	ACCAACGCGC	CTTCTACAAC	2760
TATCTGTCCG	CATGGGCCAC	CAACGACGTC	TTCGCCTACG	GAGCTTCTCA	GGGCAAATTG	2820
TATCCGGAAC	CGCGCCAGTA	TTTTACCAA	CCCAACGAGT	ACGATCTTAA	GATACCCAAG	2880
AGTCTGCCAT	TGGTCTACGC	TCAGATGCCC	TTTTACCTCC	ACGGACTAAC	AGATACCTCG	2940
CAGATCAAGA	CCCTGATAGG	TCATATTTCG	GACCTGAGCG	TCAAGTACGA	GGGCTTCGGC	3000
CTGCCCAACT	ATCCATCGGG	CATTCCCTTC	ATCTTCTGGG	AGCAGTACAT	GACCCTGCGC	3060
TCCTCACTGG	CCATGATCCT	GGCCTGCGTG	CTACTCGCCG	CCCTGGTGCT	GGTCTCCCTG	3120
CTCCTGCTCT	CCGTTTGGGC	CGCCGTTCTC	GTGATCCTCA	GCGTTCTGGC	CTCGCTGGCC	3180
CAGATCTTTG	GGGCCATGAC	TCTGCTGGGC	ATCAAACCTCT	CGGCCATTCC	GGCAGTCATA	3240
CTCATCCTCA	GCGTGGGCAT	GATGCTGTGC	TTCAATGTGC	TGATATCACT	GGGCTTCATG	3300
ACATCCGTTG	GCAACCGACA	GCGCCGCGTC	CAGCTGAGCA	TGCAGATGTC	CCTGGGACCA	3360
CTTGTCACG	GCATGCTGAC	CTCCGGAGTG	GCCGTGTTCA	TGCTCTCCAC	GTCCGCCCTT	3420
GAGTTTGTGA	TCCGGCACTT	CTGCTGGCTT	CTGCTGGTGG	TCTTATGCGT	TGGCGCCTGC	3480

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AACAGCCTTT TGGTGT C CATCCTACTG AGCATGGTGG GACCGG SC GGAGCTGGTG 3540
CCGCTGGAGC ATCCAGACCG CATATCCACG CCCTCTCCGC TGCCCGTGCG CAGCAGCAAG 3600
AGATCGGGCA AATCCTATGT GGTGCAGGGA TCGCGATCCT CGCGAGGCAG CTGCCAGAAG 3660
TCGCATCACC ACCACCACAA AGACCTTAAT GATCCATCGC TGACGACGAT CACCGAGGAG 3720
CCGCAGTCGT GGAAGTCCAG CAACTCGTCC ATCCAGATGC CCAATGATTG GACCTACCAG 3780
CCGCGGGAAC AGCGACCCGC CTCCTACGCG GCCCGGCCCC CCGCCTATCA CAAGGCCGCC 3840
GCCCAGCAGC ACCACCAGCA TCAGGGCCCG CCCACAACGC CCCC GCCTCC CTTCGCCAGC 3900
GCCTATCCGC CGGAGCTGCA GAGCATCGTG GTGCAGCCGG AGGTGACGGT GGAGACGACG 3960
CACTCGGACA GCAACACCAC CAAGGTGACG GCCACGGCCA ACATCAAGGT GGAGCTGGCC 4020
ATGCCCCGCA GGGCGGTGCG CAGCTATAAC TTTACGAGTT AGCACTAGCA CTAGTTCCTG 4080
TAGCTATTAG GACGTATCTT TAGACTCTAG CCTAAGCCGT AACCCTATTT GTATCTGTAA 4140
AATCGATTG TCCAGCGGGT CTGCTGAGGA TTTCGTTCTC ATGGATTCTC ATGGATTCTC 4200
ATGGATGCTT AAATGGCATG GTAATTGGCA AAATATCAAT TTTGTGTCT CAAAAGATG 4260
CATTAGCTTA TGGTTTCAAG ATACATTTTT AAAGAGTCCG CCAGATATTT ATATAAAAAA 4320
AATCCAAAAT CGACGTATCC ATGAAAATTG AAAAGCTAAG CAGACCCGTA TGTATGTATA 4380
TGTGTATGCA TGTTAGTTAA TTTCCCGAAG TCCGGTATTT ATAGCAGCTG CCTT 4434

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(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1285 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Met Asp Arg Asp Ser Leu Pro Arg Val Pro Asp Thr His Gly Asp Val
1          5          10          15

Val Asp Glu Lys Leu Phe Ser Asp Leu Tyr Ile Arg Thr Ser Trp Val
          20          25          30

Asp Ala Gln Val Ala Leu Asp Gln Ile Asp Lys Gly Lys Ala Arg Gly
          35          40          45

Ser Arg Thr Ala Ile Tyr Leu Arg Ser Val Phe Gln Ser His Leu Glu
50          55          60

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Thr Leu Gly 65	Ser Val Gln Lys His Ala Gly 70	Val Leu Phe Val 75	80
Ala Ile Leu Val 85	Leu Ser Thr Phe Cys Val Gly Leu Lys Ser 90	Ala Gln 95	
Ile His Ser Lys 100	Val His Gln Leu Trp Ile Gln Glu Gly Gly Arg Leu 105	110	
Glu Ala Glu Leu Ala Tyr Thr Gln Lys Thr Ile Gly Glu Asp Glu Ser 115	120	125	
Ala Thr His Gln Leu Leu Ile Gln Thr Thr His Asp Pro Asn Ala Ser 130	135	140	
Val Leu His Pro Gln Ala Leu Leu Ala His Leu Glu Val Leu Val Lys 145	150	155	160
Ala Thr Ala Val Lys Val His Leu Tyr Asp Thr Glu Trp Gly Leu Arg 165	170	175	
Asp Met Cys Asn Met Pro Ser Thr Pro Ser Phe Glu Gly Ile Tyr Tyr 180	185	190	
Ile Glu Gln Ile Leu Arg His Leu Ile Pro Cys Ser Ile Ile Thr Pro 195	200	205	
Leu Asp Cys Phe Trp Glu Gly Ser Gln Leu Leu Gly Pro Glu Ser Ala 210	215	220	
Val Val Ile Pro Gly Leu Asn Gln Arg Leu Leu Trp Thr Thr Leu Asn 225	230	235	240
Pro Ala Ser Val Met Gln Tyr Met Lys Gln Lys Met Ser Glu Glu Lys 245	250	255	
Ile Ser Phe Asp Phe Glu Thr Val Glu Gln Tyr Met Lys Arg Ala Ala 260	265	270	
Ile Gly Ser Gly Tyr Met Glu Lys Pro Cys Leu Asn Pro Leu Asn Pro 275	280	285	
Asn Cys Pro Asp Thr Ala Pro Asn Lys Asn Ser Thr Gln Pro Pro Asp 290	295	300	
Val Gly Ala Ile Leu Ser Gly Gly Cys Tyr Gly Tyr Ala Ala Lys His 305	310	315	320
Met His Trp Pro Glu Glu Leu Ile Val Gly Gly Arg Lys Arg Asn Arg 325	330	335	
Ser Gly His Leu Arg Lys Ala Gln Ala Leu Gln Ser Val Val Gln Leu 340	345	350	
Met Thr Glu Lys Glu Met Tyr Asp Gln Trp Gln Asp Asn Tyr Lys Val 355	360	365	
His His Leu Gly Trp Thr Gln Glu Lys Ala Ala Glu Val Leu Asn Ala			

Trp Gln Arg Asn Phe Ser Arg Glu Val Glu Gln Leu Leu Arg Lys Gln
385 390 395 400

Ser Arg Ile Ala Thr Asn Tyr Asp Ile Tyr Val Phe Ser Ser Ala Ala
405 410 415

Leu Asp Asp Ile Leu Ala Lys Ph Ser His Pro Ser Ala Leu Ser Ile
420 425 430

Val Ile Gly Val Ala Val Thr Val Leu Tyr Ala Phe Cys Thr Leu Leu
435 440 445

Arg Trp Arg Asp Pro Val Arg Gly Gln Ser Ser Val Gly Val Ala Gly
450 455 460

Val Leu Leu Met Cys Phe Ser Thr Ala Ala Gly Leu Gly Leu Ser Ala
465 470 475 480

Leu Leu Gly Ile Val Phe Asn Ala Leu Thr Ala Ala Tyr Ala Glu Ser
485 490 495

Asn Arg Arg Glu Gln Thr Lys Leu Ile Leu Lys Asn Ala Ser Thr Gln
500 505 510

Val Val Pro Phe Leu Ala Leu Gly Leu Gly Val Asp His Ile Phe Ile
515 520 525

Val Gly Pro Ser Ile Leu Phe Ser Ala Cys Ser Thr Ala Gly Ser Phe
530 535 540

Phe Ala Ala Ala Phe Ile Pro Val Pro Ala Leu Lys Val Phe Cys Leu
545 550 555 560

Gln Ala Ala Ile Val Met Cys Ser Asn Leu Ala Ala Ala Leu Leu Val
565 570 575

Phe Pro Ala Met Ile Ser Leu Asp Leu Arg Arg Arg Thr Ala Gly Arg
580 585 590

Ala Asp Ile Phe Cys Cys Cys Phe Pro Val Trp Lys Glu Gln Pro Lys
595 600 605

Val Ala Pro Pro Val Leu Pro Leu Asn Asn Asn Asn Gly Arg Gly Ala
610 615 620

Arg His Pro Lys Ser Cys Asn Asn Asn Arg Val Pro Leu Pro Ala Gln
625 630 635 640

Asn Pro Leu Leu Glu Gln Arg Ala Asp Ile Pro Gly Ser Ser His Ser
645 650 655

Leu Ala Ser Phe Ser Leu Ala Thr Phe Ala Phe Gln His Tyr Thr Pro
660 665 670

Phe Leu Met Arg Ser Trp Val Lys Phe Leu Thr Val Met Gly Phe Leu
675 680 685

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Ala Ala Leu Ile Ser Ser Leu Tyr Ala Ser Thr Ala Leu Gln Asp Gly
690 695 700

Leu Asp Ile Ile Asp Leu Val Pro Lys Asp Ser Asn Glu His Lys Phe
705 710 715 720

Leu Asp Ala Gln Thr Arg Leu Phe Gly Phe Tyr Ser Met Tyr Ala Val
725 730 735

Thr Gln Gly Asn Phe Glu Tyr Pro Thr Gln Gln Gln Leu Leu Arg Asp
740 745 750

Tyr His Asp Ser Phe Arg Val Pro His Val Ile Lys Asn Asp Asn Gly
755 760 765

Gly Leu Pro Asp Phe Trp Leu Leu Leu Phe Ser Glu Trp Leu Gly Asn
770 775 780

Leu Gln Lys Ile Phe Asp Glu Glu Tyr Arg Asp Gly Arg Leu Thr Lys
785 790 795 800

Glu Cys Trp Phe Pro Asn Ala Ser Ser Asp Ala Ile Leu Ala Tyr Lys
805 810 815

Leu Ile Val Gln Thr Gly His Val Asp Asn Pro Val Asp Lys Glu Leu
820 825 830

Val Leu Thr Asn Arg Leu Val Asn Ser Asp Gly Ile Ile Asn Gln Arg
835 840 845

Ala Phe Tyr Asn Tyr Leu Ser Ala Trp Ala Thr Asn Asp Val Phe Ala
850 855 860

Tyr Gly Ala Ser Gln Gly Lys Leu Tyr Pro Glu Pro Arg Gln Tyr Phe
865 870 875 880

His Gln Pro Asn Glu Tyr Asp Leu Lys Ile Pro Lys Ser Leu Pro Leu
885 890 895

Val Tyr Ala Gln Met Pro Phe Tyr Leu His Gly Leu Thr Asp Thr Ser
900 905 910

Gln Ile Lys Thr Leu Ile Gly His Ile Arg Asp Leu Ser Val Lys Tyr
915 920 925

Glu Gly Phe Gly Leu Pro Asn Tyr Pro Ser Gly Ile Pro Phe Ile Phe
930 935 940

Trp Glu Gln Tyr Met Thr Leu Arg Ser Ser Leu Ala Met Ile Leu Ala
945 950 955 960

Cys Val Leu Leu Ala Ala Leu Val Leu Val Ser Leu Leu Leu Leu Ser
965 970 975

Val Trp Ala Ala Val Leu Val Ile Leu Ser Val Leu Ala Ser Leu Ala
980 985 990

Gln Ile Phe Gly Ala Met Thr Leu Leu Gly Ile Lys Leu Ser Ala Ile

Pro Ala Val Ile Leu Ile Leu Ser Val Gly M t Met Leu Cys Phe Asn
1010 1015 1020

Val Leu Ile Ser Leu Gly Phe Met Thr Ser Val Gly Asn Arg Gln Arg
1025 1030 1035 1040

Arg Val Gln Leu Ser Met Gln Met Ser Leu Gly Pro Leu Val His Gly
1045 1050 1055

Met Leu Thr Ser Gly Val Ala Val Phe Met Leu Ser Thr Ser Pro Phe
1060 1065 1070

Glu Phe Val Ile Arg His Phe Cys Trp Leu Leu Leu Val Val Leu Cys
1075 1080 1085

Val Gly Ala Cys Asn Ser Leu Leu Val Phe Pro Ile Leu Leu Ser Met
1090 1095 1100

Val Gly Pro Glu Ala Glu Leu Val Pro Leu Glu His Pro Asp Arg Ile
1105 1110 1115 1120

Ser Thr Pro Ser Pro Leu Pro Val Arg Ser Ser Lys Arg Ser Gly Lys
1125 1130 1135

Ser Tyr Val Val Gln Gly Ser Arg Ser Ser Arg Gly Ser Cys Gln Lys
1140 1145 1150

Ser His His His His Lys Asp Leu Asn Asp Pro Ser Leu Thr Thr
1155 1160 1165

Ile Thr Glu Glu Pro Gln Ser Trp Lys Ser Ser Asn Ser Ser Ile Gln
1170 1175 1180

Met Pro Asn Asp Trp Thr Tyr Gln Pro Arg Glu Gln Arg Pro Ala Ser
1185 1190 1195 1200

Tyr Ala Ala Pro Pro Pro Ala Tyr His Lys Ala Ala Ala Gln Gln His
1205 1210 1215

His Gln His Gln Gly Pro Pro Thr Thr Pro Pro Pro Phe Pro Thr
1220 1225 1230

Ala Tyr Pro Pro Glu Leu Gln Ser Ile Val Val Gln Pro Glu Val Thr
1235 1240 1245

Val Glu Thr Thr His Ser Asp Ser Asn Thr Thr Lys Val Thr Ala Thr
1250 1255 1260

Ala Asn Ile Lys Val Glu Leu Ala Met Pro Gly Arg Ala Val Arg Ser
1265 1270 1275 1280

Tyr Asn Phe Thr Ser
1285

(2) INFORMATION FOR SEQ ID NO:7:

095403-01001

- (ii) MOLECULE TYPE: DNA (genomic).

AAGGTCCATC	AGCTTTGGAT	ACAGGAAGGT	GGTTCGCTCG	AGCATGAGCT	AGCCTACACG	60
CAGAAATCGC	TCGGCGAGAT	GGACTCCTCC	ACGCACCAGC	TGCTAATCCA	AACNCCCAA	120
GATATGGACG	CCTCGATACT	GCACCCGAAC	GCGCTACTGA	CGCACCTGGA	CGTGGTGAAG	180
AAAGCGATCT	CGGTGACGGT	GCACATGTAC	GACATCACGT	GGAGNCTCAA	GGACATGTGC	240
TACTCGCCCA	GCATACCGAG	NTTCGATACG	CACTTTATCG	AGCAGATCTT	CGAGAACATC	300
ATACCGTGCG	CGATCATCAC	GCCGCTGGAT	TGCTTTTGGG	AGGGA		345

(A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Lys	Val	His	Gln	Leu	Trp	Ile	Gln	Glu	Gly	Gly	Ser	Leu	Glu	His	Glu	
1				5					10					15		
Leu	Ala	Tyr	Thr	Gln	Lys	Ser	Leu	Gly	Glu	Met	Asp	Ser	Ser	Thr	His	
			20					25					30			
Gln	Leu	Leu	Ile	Gln	Thr	Pro	Lys	Asp	Met	Asp	Ala	Ser	Ile	Leu	His	
		35					40					45				
Pro	Asn	Ala	Leu	Leu	Thr	His	Leu	Asp	Val	Val	Lys	Lys	Ala	Ile	Ser	
	50					55					60					
Val	Thr	Val	His	Met	Tyr	Asp	Ile	Thr	Trp	Xaa	Leu	Lys	Asp	Met	Cys	
65					70					75					80	
Tyr	Ser	Pro	Ser	Ile	Pro	Xaa	Phe	Asp	Thr	His	Phe	Ile	Glu	Gln	Ile	
				85					90						95	

Phe Glu Asn 100 Ile Pro Cys Ala Ile Ile Thr 105 Leu Asp Cys Phe 110

Trp Glu Gly
115

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5187 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGTCTGTCA CCCGGAGCCG GAGTCCCCGG CGGCCAGCAG CGTCCTCGCG AGCCGAGCGC	60
CCAGGCGCGC CCGGAGCCCG CGGCGGCGGC GGCAACATGG CCTCGGCTGG TAACGCCGCC	120
GGGGCCCTGG GCAGGCAGGC CGGCGGCGGG AGGCGCAGAC GGACCGGGGG ACCGCACCGC	180
GCCGCGCCCG ACCGGGACTA TCTGCACCGG CCCAGCTACT GCGACGCCGC CTTCGCTCTG	240
GAGCAGATTT CCAAGGGGAA GGCTACTGGC CGGAAAGCGC CGCTGTGGCT GAGAGCGAAG	300
TTTCAGAGAC TCTATTAA ACTGGGTTGT TACATTCAA AGAACTGCGG CAAGTTTTTG	360
GTGTGGGTC TCCTCATATT TGGGGCCTTC GCTGTGGGAT TAAAGGCAGC TAATCTCGAG	420
ACCAACGTGG AGGAGCTGTG GGTGGAAGTT GGTGGACGAG TGAGTCGAGA ATTAAATTAT	480
ACCCGTCAGA AGATAGGAGA AGAGGCTATG TTTAATCCTC AACTCATGAT ACAGACTCCA	540
AAAGAAGAAG GCGCTAATGT TCTGACCACA GAGGCTCTCC TGCAACACCT GGAATCAGCA	600
CTCCAGGCCA GTCGTGTGCA CGTCTACATG TATAACAGGC AATGGAAGTT GGAACATTG	660
TGCTACAAAT CAGGGGAACT TATCACGGAG ACAGGTTACA TGGATCAGAT AATAGAATAC	720
CTTTACCCTT GCTTAATCAT TACACCTTG GACTGCTTCT GGGAAGGGGC AAAGCTACAG	780
TCCGGGACAG CATACTCCT AGGTAAGCCT CCTTTACGGT GGACAACTT TGACCCCTTG	840
GAATTCCTAG AAGAGTTAAA GAAATAAAC TACCAAGTGG ACAGCTGGGA GGAAATGCTG	900
AATAAGCCG AAGTTGGCCA TGGGTACATG GACCGGCCTT GCCTCAACCC AGCCGACCCA	960
GATTGCCCTG CCACAGCCCC TAACAAAAAT TCAACCAAAC CTCTTGATGT GGCCCTTGTT	1020
TTGAATGGTG GATGTCAAGG TTTATCCAGG AAGTATATGC ATTGGCAGGA GGAGTTGATT	1080
GTGGGTGGTA CCGTCAAGAA TGCCACTGGA AAAGTTGTCA GCGCTCACGC CCTGCAAACC	1140

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ATGTTCCAGT TAATGA CAAGCAAATG TATGAACACT TCAGGG	CGACTATGTC	1200
TCTCACATCA ACTGGAATGA AGACAGGGCA GCCGCCATCC TGGAGGCCTG GCAGAGGACT		1260
TACGTGGAGG TGGTTCATCA AAGTGTGCGC CCAAACCTCCA CTCAAAAGGT GCTTCCCTTC		1320
ACAACCACGA CCCTGGACGA CATCCTAAAA TCCTTCTCTG ATGTCAGTGT CATCCGAGTG		1380
GCCAGCGGCT ACCTACTGAT GCTTGCCTAT GCCTGTTTAA CCATGCTGCG CTGGGACTGC		1440
TCCAAGTCCC AGGGTGCCGT GGGGCTGGCT GCGCTCCTGT TGGTTGCGCT GTCAGTGGCT		1500
GCAGGATTGG GCCTCTGCTC CTTGATTGGC ATTTCTTTTA ATGCTGCGAC AACTCAGGTT		1560
TTGCCGTTTC TTGCTCTTGG TGTGGTGTG GATGATGTCT TCCTCCTGGC CCATGCATTC		1620
AGTGAAACAG GACAGAATAA GAGGATTCCA TTTGAGGACA GGAAGTGGGA GTGCCTCAAG		1680
CGCACCAGGAG CCAGCGTGGC CCTCACCTCC ATCAGCAATG TCACCGCCTT CTCATGGCC		1740
GCATTGATCC CTATCCCTGC CCTGCGAGCG TTCTCCCTCC AGGCTGCTGT GGTGGTGGTA		1800
TTCAATTTTG CTATGGTTCT GCTCATTTTT CCTGCAATTC TCAGCATGGA TTTATACAGA		1860
CGTGAGGACA GAAGATTGGA TATTTTCTGC TGTTTCACAA GCCCCTGTGT CAGCAGGGTG		1920
ATTCAAGTTG AGCCACAGGC CTACACAGAG CCTCACAGTA ACACCCGGTA CAGCCCCCA		1980
CCCCCATACA CCAGCCACAG CTTGCCCCAC GAAACCCATA TCACTATGCA GTCCACCGTT		2040
CAGCTCCGCA CAGAGTATGA CCCTCACAG CACGTGTACT ACACCACCGC CGAGCCACGC		2100
TCTGAGATCT CTGTACAGCC TGTTACCGTC ACCCAGGACA ACCTCAGCTG TCAGAGTCCC		2160
GAGAGCACCA GCTCTACCAG GGACCTGCTC TCCCAGTTCT CAGACTCCAG CCTCCACTGC		2220
CTCGAGCCCC CCTGCACCAA GTGGACACTC TCTTCGTTTG CAGAGAAGCA CTATGCTCCT		2280
TTCTCCTGA AACCCAAAGC CAAGGTTGTG GTAATCCTTC TTTTCCTGGG CTTGCTGGGG		2340
GTCAGCCTTT ATGGGACCAC CCGAGTGAGA GACGGGCTGG ACCTCACGGA CATTGTTCCC		2400
CGGGAAACCA GAGAATATGA CTTCATAGCT GCCCAGTTCA AGTACTTCTC TTTCTACAAC		2460
ATGTATATAG TCACCCAGAA AGCAGACTAC CCGAATATCC AGCACCTACT TTACGACCTT		2520
CATAAGAGTT TCAGCAATGT GAAGTATGTC ATGCTGGAGG AGAACAAGCA ACTTCCCCAA		2580
ATGTGGCTGC ACTACTTTAG AGACTGGCTT CAAGGACTTC AGGATGCATT TGACAGTGAC		2640
TGGGAAACTG GGAGGATCAT GCCAAACAAT TATAAAAATG GATCAGATGA CGGGGTCCTC		2700
GCTTACAAAC TCCTGGTGCA GACTGGCAGC CGAGACAAGC CCATCGACAT TAGTCAGTTG		2760
ACTAAACAGC GTCTGGTAGA CGCAGATGGC ATCATTAAATC CGAGCGCTTT CTACATCTAC		2820
CTGACCGCTT GGGTCAGCAA CGACCCTGTA GCTTACGCTG CCTCCCAGGC CAACATCCGG		2880

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CCTCACCGGC CGGAGT	CCATGACAAA GCCGACTACA TGCCAC	CAGGCTGAGA	2940
ATCCCAGCAG CAGAGCCCAT	CGAGTACGCT CAGTTCCCTT TCTACCTCAA	CGGCCTACGA	3000
GACACCTCAG ACTTTGTGGA	AGCCATAGAA AAAGTGAGAG TCATCTGTAA	CAACTATACG	3060
AGCCTGGGAC TGTCCAGCTA	CCCCAATGGC TACCCCTTCC TGTTCTGGGA	GCAATACATC	3120
AGCCTGCGCC ACTGGCTGCT	GCTATCCATC AGCGTGGTGC TGGCCTGCAC	GTTTCTAGTG	3180
TGCGCAGTCT TCCTCCTGAA	CCCCTGGACG GCCGGGATCA TTGTCATGGT	CCTGGCTCTG	3240
ATGACCGTTG AGCTCTTTGG	CATGATGGGC CTCATTGGGA TCAAGCTGAG	TGCTGTGCCT	3300
GTGGTCATCC TGATTGCATC	TGTTGGCATC GGAGTGGAGT TCACCGTCCA	CGTGGCTTTG	3360
GCCTTTCTGA CAGCCATTGG	GGACAAGAAC CACAGGGCTA TGCTCGCTCT	GGAACACATG	3420
TTTGCTCCCG TTCTGGACGG	TGCTGTGTCC ACTCTGCTGG GTGTACTGAT	GCTTGCAGGG	3480
TCCGAATTG ATTTTCATTGT	CAGATACTTC TTTGCCGTCC TGGCCATTCT	CACCGTCTTG	3540
GGGGTTCTCA ATGGACTGGT	TCTGCTGCCT GTCCTCTTAT CCTTCTTTGG	ACCGTGTCTT	3600
GAGGTGTCTC CAGCCAATGG	CCTAAACCGA CTGCCCACTC CTTGCGCTGA	GCCGCCTCCA	3660
AGTGTCGTCC GGTTTGCCGT	GCCTCCTGGT CACACGAACA ATGGGTCTGA	TTCCTCCGAC	3720
TCGGAGTACA GCTCTCAGAC	CACGGTGTCT GGCATCAGTG AGGAGCTCAG	GCAATACGAA	3780
GCACAGCAGG GTGCCGGAGG	CCCTGCCCCAC CAAGTGATTG TGGAAGCCAC	AGAAAACCCT	3840
GTCTTTGCCC GGTCCACTGT	GGTCCATCCG GACTCCAGAC ATCAGCCTCC	CTTGACCCCT	3900
CGGCAACAGC CCCACCTGGA	CTCTGGCTCC TTGTCCCCTG GACGGCAAGG	CCAGCAGCCT	3960
CGAAGGGATC CCCCTAGAGA	AGGCTTGCGG CCACCCCCCT ACAGACCGCG	CAGAGACGCT	4020
TTTGAAATTT CTACTIONAAG	GCATTCTGGC CCTAGCAATA GGGACCGCTC	AGGGCCCCGT	4080
GGGGCCCCGT CTCACAACCC	TCGGAACCCA ACGTCCACCG CCATGGGCAG	CTCTGTGCCC	4140
AGCTACTGCC AGCCCATCAC	CACTGTGACG GCTTCTGCTT CGGTGACTGT	TGCTGTGCAT	4200
CCCCCGCCTG GACCTGGGCG	CAACCCCCGA GGGGGGCCCT GTCCAGGCTA	TGAGAGCTAC	4260
CCTGAGACTG ATCACGGGGT	ATTGAGGAT CCTCATGTGC CTTTTCATGT	CAGGTGTGAG	4320
AGGAGGGACT CAAAGGTGGA	GGTCATAGAG CTACAGGACG TGGAATGTGA	GGAGAGGCCG	4380
TGGGGGAGCA GCTCCAACCTG	AGGGTAATTA AAATCTGAAG CAAAGAGGCC	AAAGATTGGA	4440
AAGCCCCGCC CCCACCTCTT	TCCAGAACTG CTTGAAGAGA ACTGCTTGGA	ATTATGGGAA	4500
GGCAGTTCAT TGTTACTGTA	ACTGATTGTA TTATTKKGTG AAATATTTCT	ATAAATATTT	4560
AARAGGTGTA CACATGTAAT	ATACATGGAA ATGCTGTACA GTCTATTTCC	TGGGGCCTCT	4620

CCACTCCTGC CCCAGAC GGAGACCACA GGGGCCCTTT CCCCTG CATTGGTCTC 4680
 TGTGCCACAA CCAAGCTTAA CTTAGTTTTA AAAAAATCT CCCAGCATAT GTCGCTGCTG 4740
 CTAAATATT GTATAATTTA CTTGTATAAT TCTATGCAAA TATTGCTTAT GTAATAGGAT 4800
 TATTTGTAAA GGTTTCTGTT TAAATATTT TAAATTTGCA TATCACAACC CTGTGGTAGG 4860
 ATGAATTGTT ACTGTAACT TTTGAACACG CTATGCGTGG TAATTGTTTA ACGAGCAGAC 4920
 ATGAAGAAAA CAGGTTAATC CCAGTGGCTT CTCTAGGGGT AGTTGTATAT GGTTCGCATG 4980
 GGTGGATGTG TGTGTGCATG TGA CTTTCCA ATGTACTGTA TTGTGGTTTG TTGTTGTTGT 5040
 TGCTGTTGTT GTTCATTTTG GTGTTTTTGG TTGCTTTGTA TGATCTTAGC TCTGGCCTAG 5100
 GTGGGCTGGG AAGGTCCAGG TCTTTTTCTG TCGTGATGCT GGTGGAAAGG TGACCCCAAT 5160
 CATCTGTCCT ATTCTCTGGG ACTATTC 5187

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1434 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ala Ser Ala Gly Asn Ala Ala Gly Ala Leu Gly Arg Gln Ala Gly
 1 5 10 15
 Gly Gly Arg Arg Arg Arg Thr Gly Gly Pro His Arg Ala Ala Pro Asp
 20 25 30
 Arg Asp Tyr Leu His Arg Pro Ser Tyr Cys Asp Ala Ala Phe Ala Leu
 35 40 45
 Glu Gln Ile Ser Lys Gly Lys Ala Thr Gly Arg Lys Ala Pro Leu Trp
 50 55 60
 Leu Arg Ala Lys Phe Gln Arg Leu Leu Phe Lys Leu Gly Cys Tyr Ile
 65 70 75 80
 Gln Lys Asn Cys Gly Lys Phe Leu Val Val Gly Leu Leu Ile Phe Gly
 85 90 95
 Ala Phe Ala Val Gly Leu Lys Ala Ala Asn Leu Glu Thr Asn Val Glu
 100 105 110
 Glu Leu Trp Val Glu Val Gly Gly Arg Val Ser Arg Glu Leu Asn Tyr
 115 120 125

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Thr Arg Gln Ile Gly Glu Glu Ala Met Phe Asn Gln Leu Met
 130 135 140

Ile Gln Thr Pro Lys Glu Glu Gly Ala Asn Val Leu Thr Thr Glu Ala
 145 150 155 160

Leu Leu Gln His Leu Asp Ser Ala Leu Gln Ala Ser Arg Val His Val
 165 170 175

Tyr Met Tyr Asn Arg Gln Trp Lys Leu Glu His Leu Cys Tyr Lys Ser
 180 185 190

Gly Glu Leu Ile Thr Glu Thr Gly Tyr Met Asp Gln Ile Ile Glu Tyr
 195 200 205

Leu Tyr Pro Cys Leu Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly
 210 215 220

Ala Lys Leu Gln Ser Gly Thr Ala Tyr Leu Leu Gly Lys Pro Pro Leu
 225 230 235 240

Arg Trp Thr Asn Phe Asp Pro Leu Glu Phe Leu Glu Glu Leu Lys Lys
 245 250 255

Ile Asn Tyr Gln Val Asp Ser Trp Glu Glu Met Leu Asn Lys Ala Glu
 260 265 270

Val Gly His Gly Tyr Met Asp Arg Pro Cys Leu Asn Pro Ala Asp Pro
 275 280 285

Asp Cys Pro Ala Thr Ala Pro Asn Lys Asn Ser Thr Lys Pro Leu Asp
 290 295 300

Val Ala Leu Val Leu Asn Gly Gly Cys Gln Gly Leu Ser Arg Lys Tyr
 305 310 315 320

Met His Trp Gln Glu Glu Leu Ile Val Gly Gly Thr Val Lys Asn Ala
 325 330 335

Thr Gly Lys Leu Val Ser Ala His Ala Leu Gln Thr Met Phe Gln Leu
 340 345 350

Met Thr Pro Lys Gln Met Tyr Glu His Phe Arg Gly Tyr Asp Tyr Val
 355 360 365

Ser His Ile Asn Trp Asn Glu Asp Arg Ala Ala Ala Ile Leu Glu Ala
 370 375 380

Trp Gln Arg Thr Tyr Val Glu Val Val His Gln Ser Val Ala Pro Asn
 385 390 395 400

Ser Thr Gln Lys Val Leu Pro Phe Thr Thr Thr Thr Leu Asp Asp Ile
 405 410 415

Leu Lys Ser Phe Ser Asp Val Ser Val Ile Arg Val Ala Ser Gly Tyr
 420 425 430

Leu Leu Met Leu Ala Tyr Ala Cys Leu Thr Met Leu Arg Trp Asp Cys

S r Lys Ser Gln Gly Ala Val Gly Leu Ala Gly Val Leu Leu Val Ala
450 455 460

Leu Ser Val Ala Ala Gly Leu Gly Leu Cys Ser Leu Ile Gly Ile Ser
465 470 475 480

Phe Asn Ala Ala Thr Thr Gln Val Leu Pro Phe Leu Ala Leu Gly Val
485 490 495

Gly Val Asp Asp Val Phe Leu Leu Ala His Ala Phe Ser Glu Thr Gly
500 505 510

Gln Asn Lys Arg Ile Pro Phe Glu Asp Arg Thr Gly Glu Cys Leu Lys
515 520 525

Arg Thr Gly Ala Ser Val Ala Leu Thr Ser Ile Ser Asn Val Thr Ala
530 535 540

Phe Phe Met Ala Ala Leu Ile Pro Ile Pro Ala Leu Arg Ala Phe Ser
545 550 555 560

Leu Gln Ala Ala Val Val Val Val Phe Asn Phe Ala Met Val Leu Leu
565 570 575

Ile Phe Pro Ala Ile Leu Ser Met Asp Leu Tyr Arg Arg Glu Asp Arg
580 585 590

Arg Leu Asp Ile Phe Cys Cys Phe Thr Ser Pro Cys Val Ser Arg Val
595 600 605

Ile Gln Val Glu Pro Gln Ala Tyr Thr Glu Pro His Ser Asn Thr Arg
610 615 620

Tyr Ser Pro Pro Pro Pro Tyr Thr Ser His Ser Phe Ala His Glu Thr
625 630 635 640

His Ile Thr Met Gln Ser Thr Val Gln Leu Arg Thr Glu Tyr Asp Pro
645 650 655

His Thr His Val Tyr Tyr Thr Thr Ala Glu Pro Arg Ser Glu Ile Ser
660 665 670

Val Gln Pro Val Thr Val Thr Gln Asp Asn Leu Ser Cys Gln Ser Pro
675 680 685

Glu Ser Thr Ser Ser Thr Arg Asp Leu Leu Ser Gln Phe Ser Asp Ser
690 695 700

Ser Leu His Cys Leu Glu Pro Pro Cys Thr Lys Trp Thr Leu Ser Ser
705 710 715 720

Phe Ala Glu Lys His Tyr Ala Pro Phe Leu Leu Lys Pro Lys Ala Lys
725 730 735

Val Val Val Ile Leu Leu Phe Leu Gly Leu Leu Gly Val Ser Leu Tyr
740 745 750

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Gly Thr Thr Ala Val Arg Asp Gly Leu Asp Leu Thr Ile Val Pro
755 760 765

Arg Glu Thr Arg Glu Tyr Asp Phe Ile Ala Ala Gln Phe Lys Tyr Phe
770 775 780

Ser Phe Tyr Asn Met Tyr Ile Val Thr Gln Lys Ala Asp Tyr Pro Asn
785 790 795 800

Ile Gln His Leu Leu Tyr Asp Leu His Lys Ser Phe Ser Asn Val Lys
805 810 815

Tyr Val Met Leu Glu Glu Asn Lys Gln Leu Pro Gln Met Trp Leu His
820 825 830

Tyr Phe Arg Asp Trp Leu Gln Gly Leu Gln Asp Ala Phe Asp Ser Asp
835 840 845

Trp Glu Thr Gly Arg Ile Met Pro Asn Asn Tyr Lys Asn Gly Ser Asp
850 855 860

Asp Gly Val Leu Ala Tyr Lys Leu Leu Val Gln Thr Gly Ser Arg Asp
865 870 875 880

Lys Pro Ile Asp Ile Ser Gln Leu Thr Lys Gln Arg Leu Val Asp Ala
885 890 895

Asp Gly Ile Ile Asn Pro Ser Ala Phe Tyr Ile Tyr Leu Thr Ala Trp
900 905 910

Val Ser Asn Asp Pro Val Ala Tyr Ala Ala Ser Gln Ala Asn Ile Arg
915 920 925

Pro His Arg Pro Glu Trp Val His Asp Lys Ala Asp Tyr Met Pro Glu
930 935 940

Thr Arg Leu Arg Ile Pro Ala Ala Glu Pro Ile Glu Tyr Ala Gln Phe
945 950 955 960

Pro Phe Tyr Leu Asn Gly Leu Arg Asp Thr Ser Asp Phe Val Glu Ala
965 970 975

Ile Glu Lys Val Arg Val Ile Cys Asn Asn Tyr Thr Ser Leu Gly Leu
980 985 990

Ser Ser Tyr Pro Asn Gly Tyr Pro Phe Leu Phe Trp Glu Gln Tyr Ile
995 1000 1005

Ser Leu Arg His Trp Leu Leu Leu Ser Ile Ser Val Val Leu Ala Cys
1010 1015 1020

Thr Phe Leu Val Cys Ala Val Phe Leu Leu Asn Pro Trp Thr Ala Gly
1025 1030 1035 1040

Ile Ile Val Met Val Leu Ala Leu Met Thr Val Glu Leu Phe Gly Met
1045 1050 1055

Met Gly Leu Ile Gly Ile Lys Leu Ser Ala Val Pro Val Val Ile Leu

Ile Ala Ser Val Gly Ile Gly Val Glu Phe Thr Val His Val Ala Leu
 1075 1080 1085
 Ala Phe Leu Thr Ala Ile Gly Asp Lys Asn His Arg Ala Met Leu Ala
 1090 1095 1100
 Leu Glu His Met Phe Ala Pro Val Leu Asp Gly Ala Val Ser Thr Leu
 1105 1110 1115 1120
 Leu Gly Val Leu Met Leu Ala Gly Ser Glu Phe Asp Phe Ile Val Arg
 1125 1130 1135
 Tyr Phe Phe Ala Val Leu Ala Ile Leu Thr Val Leu Gly Val Leu Asn
 1140 1145 1150
 Gly Leu Val Leu Leu Pro Val Leu Leu Ser Phe Phe Gly Pro Cys Pro
 1155 1160 1165
 Glu Val Ser Pro Ala Asn Gly Leu Asn Arg Leu Pro Thr Pro Ser Pro
 1170 1175 1180
 Glu Pro Pro Pro Ser Val Val Arg Phe Ala Val Pro Pro Gly His Thr
 1185 1190 1195 1200
 Asn Asn Gly Ser Asp Ser Ser Asp Ser Glu Tyr Ser Ser Gln Thr Thr
 1205 1210 1215
 Val Ser Gly Ile Ser Glu Glu Leu Arg Gln Tyr Glu Ala Gln Gln Gly
 1220 1225 1230
 Ala Gly Gly Pro Ala His Gln Val Ile Val Glu Ala Thr Glu Asn Pro
 1235 1240 1245
 Val Phe Ala Arg Ser Thr Val Val His Pro Asp Ser Arg His Gln Pro
 1250 1255 1260
 Pro Leu Thr Pro Arg Gln Gln Pro His Leu Asp Ser Gly Ser Leu Ser
 1265 1270 1275 1280
 Pro Gly Arg Gln Gly Gln Gln Pro Arg Arg Asp Pro Pro Arg Glu Gly
 1285 1290 1295
 Leu Arg Pro Pro Pro Tyr Arg Pro Arg Asp Ala Phe Glu Ile Ser
 1300 1305 1310
 Thr Glu Gly His Ser Gly Pro Ser Asn Arg Asp Arg Ser Gly Pro Arg
 1315 1320 1325
 Gly Ala Arg Ser His Asn Pro Arg Asn Pro Thr Ser Thr Ala Met Gly
 1330 1335 1340
 Ser Ser Val Pro Ser Tyr Cys Gln Pro Ile Thr Thr Val Thr Ala Ser
 1345 1350 1355 1360
 Ala Ser Val Thr Val Ala Val His Pro Pro Pro Gly Pro Gly Arg Asn
 1365 1370 1375

Pro Arg Gly G Pro Cys Pro Gly Tyr Glu Ser Ty Pro Glu Thr Asp
 1380 1385 1390

His Gly Val Phe Glu Asp Pro His Val Pro Phe His Val Arg Cys Glu
 1395 1400 1405

Arg Arg Asp Ser Lys Val Glu Val Ile Glu Leu Gln Asp Val Glu Cys
 1410 1415 1420

Glu Glu Arg Pro Trp Gly Ser Ser Ser Asn
 1425 1430

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Leu Ile Val Gly Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Pro Phe Phe Trp Glu Gln Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGACGAATTC AARGTNCAVC ARYTNTGG

28

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGACGAATTC CYTCCCARAA RCANTC

26

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CATACCAGCC AAGCTTGTCN GGCCARTGCA T

31

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTCCGGG GACCGCAAGG AGTGCCGCGG AAGCGCCCGA AGGACAGGCT CGCTCGGCGC	60
GCCGGCTCTC GCTCTTCCGC GAACTGGATG TGGGCAGCGG CGGCCGAGA GACCTCGGGA	120
CCCCCGCGCA ATGTGGCAAT GGAAGGCGCA GGGTCTGACT CCCCAGCAGC GGCCGCGGCC	180
GCAGCGGCAG CAGCGCCCGC CGTGTGAGCA GCAGCAGCGG CTGGTCTGTC AACCGGAGCC	240
CGAGCCCGAG CAGCCTGCGG CCAGCAGCGT CCTCGCAAGC CGAGCGCCCA GCGCGGCCAG	300
GAGCCCGCAG CAGCGGCAGC AGCGCGCCGG GCCGCCCGGG AAGCCTCCGT CCCCAGGACC	360
GCGGCGGCGG CGGCGGCGGC AACATGGCCT CGGCTGGTAA CGCCGCCGAG CCCCAGGACC	420
GCGGCGGCGG CGGCGGCGGC TGTATCGGTG CCCCAGGACG GCCGGCTGGA GCGGGGAGGC	480
GCAGACGGAC GGGGGGGCTG CGCCGTGCTG CCGCGCCGGA CCGGGACTAT CTGCACCGGC	540
CCAGCTACTG CGACGCCGCC TTCGCTCTGG AGCAGATTTC CAAGGGGAAG GCTACTGGCC	600
GGAAAGCGCC ACTGTGGCTG AGAGCGAAGT TTCAGAGACT CTTATTATAA CTGGGTGTT	660
ACATTCAAAA AAAGTGGGC AAGTTCTTGG TTGTGGGCCT CCTCATATTT GGGGCCTTCG	720

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CGGTGGGATT AAAAGCA AACCTCGAGA CCAACGTGGA GGAGCTG GTGGAAGTTG	780
GAGGACGAGT AAGTCGTGAA TTAAATTATA CTCGCCAGAA GATTGGAGAA GAGGCTATGT	840
TTAATCCTCA ACTCATGATA CAGACCCCTA AAGAAGAAGG TGCTAATGTC CTGACCACAG	900
AAGCGCTCCT ACAACACCTG GACTCGGCAC TCCAGGCCAG CCGTGTCCAT GTATACATGT	960
ACAACAGGCA GTGGAAATTG GAACATTTGT GTTACAAATC AGGAGAGCTT ATCACAGAAA	1020
CAGGTTACAT GGATCAGATA ATAGAATATC TTTACCCTTG TTTGATTATT ACACCTTTGG	1080
ACTGCTTCTG GGAAGGGGCG AAATTACAGT CTGGGACAGC ATACCTCCTA GGTAAACCTC	1140
CTTTGCGGTG GACAACTTC GACCCTTTGG AATTCCTGGA AGAGTTAAAG AAAATAAACT	1200
ATCAAGTGGA CAGCTGGGAG GAAATGCTGA ATAAGGCTGA GGTGGTTCAT GGTACATGG	1260
ACCGCCCCTG CCTCAATCCG GCCGATCCAG ACTGCCCCGC CACAGCCCCC AACAAAAATT	1320
CAACCAAACC TCTTGATATG GCCCTTGTTT TGAATGGTGG ATGTCATGGC TTATCCAGAA	1380
AGTATATGCA CTGGCAGGAG GAGTTGATTG TGGGTGGCAC AGTCAAGAAC AGCACTGGAA	1440
AACTCGTCAG CGCCCATGCC CTGCAGACCA TGTTCAGTT AATGACTCCC AAGCAAATGT	1500
ACGAGCACTT CAAGGGGTAC GAGTATGTCT CACACATCAA CTGGAACGAG GACAAAGCGG	1560
CAGCCATCCT GGAGGCCTGG CAGAGGACAT ATGTGGAGGT GGTTCATCAG AGTGTGCGAC	1620
AGAACTCCAC TCAAAAGGTG CTTTCCTTCA CCACCACGAC CCTGGACGAC ATCCTGAAAT	1680
CCTTCTCTGA CGTCAGTGTC ATCCGCGTGG CCAGCGGCTA CTTACTCATG CTCGCCTATG	1740
CCTGTCTAAC CATGCTGCGC TGGGACTGCT CCAAGTCCCA GGGTGCCGTG GGGCTGGCTG	1800
GCGTCCTGCT GGTGCACTG TCAGTGGCTG CAGGACTGGG CCTGTGCTCA TTGATCGGAA	1860
TTTCCTTTAA CGCTGCAACA ACTCAGGTTT TGCCATTTCT CGCTCTTGGT GTTGGTGTGG	1920
ATGATGTTTT TCTTCTGGCC CACGCCTTCA GTGAAACAGG ACAGAATAAA AGAATCCCTT	1980
TTGAGGACAG GACCGGGGAG TGCCTGAAGC GCACAGGAGC CAGCGTGGCC CTCACGTCCA	2040
TCAGCAATGT CACAGCCTTC TTCATGGCCG CGTTAATCCC AATCCCGCT CTGCGGGCGT	2100
TCTCCCTCCA GGCAGCGGTA GTAGTGGTGT TCAATTTTGC CATGGTTCTG CTCATTTTTT	2160
CTGCAATTCT CAGCATGGAT TTATATCGAC GCGAGGACAG GAGACTGGAT ATTTTCTGCT	2220
GTTTTACAAG CCCCTGCGTC AGCAGAGTGA TTCAGGTTGA ACCTCAGGCC TACACCGACA	2280
CACACGACAA TACCCGCTAC AGCCCCCAC CTCCCTACAG CAGCCACAGC TTTGCCCATG	2340
AAACGCAGAT TACCATGCAG TCCACTGTCC AGCTCCGCAC GGAGTACGAC CCCCACACGC	2400
ACGTGTACTA CACCACCGCT GAGCCGCGCT CCGAGATCTC TGTGCAGCCC GTCACCGTGA	2460

CACAGGACAC CCTCAGC CAGAGCCCAG AGAGCACCAG CTCCACA GACCTGCTCT	2520
CCCAGTTCTC CGACTCCAGC CTCCACTGCC TCGAGCCCCC CTGTACGAAG TGGACACTCT	2580
CATCTTTTGC TGAGAAGCAC TATGCTCCTT TCCTCTTGAA ACCAAAAGCC AAGGTAGTGG	2640
TGATCTTCCT TTTTCTGGGC TTGCTGGGGG TCAGCCTTTA TGGCACCACC CGAGTGAGAG	2700
ACGGGCTGGA CCTTACGGAC ATTGTACCTC GGGAAACCAG AGAATATGAC TTTATTGCTG	2760
CACAATTCAA ATACTTTTCT TTCTACAACA TGTATATAGT CACCCAGAAA GCAGACTACC	2820
CGAATATCCA GCACTTACTT TACGACCTAC ACAGGAGTTT CAGTAACGTG AAGTATGTCA	2880
TGTTGGAAGA AAACAAACAG CTTCCCAAAA TGTGGCTGCA CTACTTCAGA GACTGGCTTC	2940
AGGGACTTCA GGATGCATTT GACAGTGA CT GGGAAACCGG GAAAATCATG CCAAACAATT	3000
ACAAGAATGG ATCAGACGAT GGAGTCCTTG CCTACAAACT CCTGGTGCAA ACCGGCAGCC	3060
GCGATAAGCC CATCGACATC AGCCAGTTGA CTAAACAGCG TCTGGTGGAT GCAGATGGCA	3120
TCATTAATCC CAGCGCTTTC TACATCTACC TGACGGCTTG GGTCAGCAAC GACCCCGTCG	3180
CGTATGCTGC CTCCCAGGCC AACATCCGGC CACACCGACC AGAATGGGTC CACGACAAAG	3240
CCGACTACAT GCCTGAAACA AGGCTGAGAA TCCCGGCAGC AGAGCCCATC GAGTATGCCC	3300
AGTTCCCTTT CTACCTCAAC GGGTTGCGGG ACACCTCAGA CTTTGTGGAG GCAATTGAAA	3360
AAGTAAGGAC CATCTGCAGC AACTATACGA GCCTGGGGCT GTCCAGTTAC CCCAACGGCT	3420
ACCCCTTCCT CTTCTGGGAG CAGTACATCG GCCTCCGCCA CTGGCTGCTG CTGTTCATCA	3480
GCGTGGTGTT GGCCTGCACA TTCCTCGTGT GCGCTGTCTT CTTTCTGAAC CCCTGGACGG	3540
CCGGGATCAT TGTGATGGTC CTGGCGCTGA TGACGGTCGA GCTGTTCGGC ATGATGGGCC	3600
TCATCGGAAT CAAGCTCAGT GCCGTGCCCC TGGTCATCCT GATCGCTTCT GTTGGCATAG	3660
GAGTGGAGTT CACCGTTCAC GTTGCTTTGG CCTTTCTGAC GGCCATCGGC GACAAGAACC	3720
GCAGGGCTGT GCTTGCCCTG GAGCACATGT TTGCACCCGT CCTGGATGGC GCCGTGTCCA	3780
CTCTGCTGGG AGTGCTGATG CTGGCGGGAT CTGAGTTCGA CTTCAATTGTC AGGTATTTCT	3840
TTGCTGTGCT GGCGATCCTC ACCATCCTCG GCGTTCTCAA TGGGCTGGTT TTGCTTCCCG	3900
TGCTTTTGTC TTTCTTTGGA CCATATCCTG AGGTGTCTCC AGCCAACGGC TTGAACCGCC	3960
TGCCCCACACC CTCCCCTGAG CCACCCCCCA GCGTGGTCCG CTTGCCCATG CCGCCCGGCC	4020
ACACGCACAG CGGGTCTGAT TCCTCCGACT CGGAGTATAG TTCCCAGACG ACAGTGTGAG	4080
GCCTCAGCGA GGAGCTTCGG CACTACGAGG CCCAGCAGGG CGCGGGAGGC CCTGCCCCACC	4140
AAGTGATCGT GGAAGCCACA GAAAACCCCG TCTTCGCCCA CTCCACTGTG GTCCATCCCC	4200

AATCCAGGCA TCACCGC TCGAACCCGA GACAGCAGCC CCACCTGGAC TCAGGGTCCC 4260
 TGCCTCCCGG ACGGCAAGGC CAGCAGCCCC GCAGGGACCC CCCCAGAGAA GGCTTGTGGC 4320
 CACCCCTCTA CAGACCGCGC AGAGACGCTT TTGAAATTTT TACTGAAGGG CATTCTGGCC 4380
 CTAGCAATAG GGCCCGCTGG GGCCCTCGCG GGGCCCGTTC TCACAACCCT CGGAACCCAG 4440
 CGTCCACTGC CATGGGCAGC TCCGTGCCCC GCTACTGCCA GCCCATCACC ACTGTGACGG 4500
 CTTCTGCCTC CGTGACTGTC GCGGTGCACC CGCCGCCTGT CCCTGGGCCT GGGCGGAACC 4560
 CCCGAGGGGG ACTCTGCCCA GGCTACCCTG AGACTGACCA CGGCCTGTTT GAGGACCCCC 4620
 ACGTGCCTTT CCACGTCCGG TGTGAGAGGA GGGATTGAA GGTGGAAGTC ATTGAGCTGC 4680
 AGGACGTGGA ATGCGAGGAG AGGCCCCGGG GAAGCAGCTC CAACTGAGGG TGATTAAAT 4740
 CTGAAGCAA GAGGCCAAAG ATTGGAAACC CCCCACCCCC ACCTCTTTCC AGAACTGCTT 4800
 GAAGAGAACT GGTGGAGTT ATGGAAAAGA TGCCCTGTGC CAGGACAGCA GTTCATTGTT 4860
 ACTGTAACCG ATTGTATTAT TTTGTTAAAT ATTTCTATAA ATATTTAAGA GATGTACACA 4920
 TGTGTAATAT AGGAAGGAAG GATGTAAAGT GGTATGATCT GGGGCTTCTC CACTCCTGCC 4980
 CCAGAGTGTG GAGGCCACAG TGGGGCCTCT CCGTATTTGT GCATTGGGCT CCGTGCCACA 5040
 ACCAAGCTTC ATTAGTCTTA AATTTAGCA TATGTTGCTG CTGCTTAAAT ATTGTATAAT 5100
 TTACTTGTAT AATTCTATGC AAATATTGCT TATGTAATAG GATTATTTTG TAAAGGTTTC 5160
 TGTTTAAAT ATTTTAAATT TGCATATCAC AACCCGTGG TAGTATGAAA TGTTACTGTT 5220
 AACTTTCAAA CACGCTATGC GTGATAATTT TTTTGTTTAA TGAGCAGATA TGAAGAAAGC 5280
 CCGGAATT 5288

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1447 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Ala Ser Ala Gly Asn Ala Ala Glu Pro Gln Asp Arg Gly Gly Gly
 1 5 10 15
 Gly Ser Gly Cys Ile Gly Ala Pro Gly Arg Pro Ala Gly Gly Gly Arg
 20 25 30

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Arg Arg Arg 35 Gly Gly Leu Arg Arg Ala Ala A 40 Pro Asp Arg Asp 45
Tyr Leu His Arg Pro Ser Tyr Cys Asp Ala Ala Phe Ala Leu Glu Gln 50 55 60
Ile Ser Lys Gly Lys Ala Thr Gly Arg Lys Ala Pro Leu Trp Leu Arg 65 70 75 80
Ala Lys Phe Gln Arg Leu Leu Phe Lys Leu Gly Cys Tyr Ile Gln Lys 85 90 95
Asn Cys Gly Lys Phe Leu Val Val Gly Leu Leu Ile Phe Gly Ala Phe 100 105 110
Ala Val Gly Leu Lys Ala Ala Asn Leu Glu Thr Asn Val Glu Glu Leu 115 120 125
Trp Val Glu Val Gly Gly Arg Val Ser Arg Glu Leu Asn Tyr Thr Arg 130 135 140
Gln Lys Ile Gly Glu Glu Ala Met Phe Asn Pro Gln Leu Met Ile Gln 145 150 155 160
Thr Pro Lys Glu Glu Gly Ala Asn Val Leu Thr Thr Glu Ala Leu Leu 165 170 175
Gln His Leu Asp Ser Ala Leu Gln Ala Ser Arg Val His Val Tyr Met 180 185 190
Tyr Asn Arg Gln Trp Lys Leu Glu His Leu Cys Tyr Lys Ser Gly Glu 195 200 205
Leu Ile Thr Glu Thr Gly Tyr Met Asp Gln Ile Ile Glu Tyr Leu Tyr 210 215 220
Pro Cys Leu Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly Ala Lys 225 230 235 240
Leu Gln Ser Gly Thr Ala Tyr Leu Leu Gly Lys Pro Pro Leu Arg Trp 245 250 255
Thr Asn Phe Asp Pro Leu Glu Phe Leu Glu Glu Leu Lys Lys Ile Asn 260 265 270
Tyr Gln Val Asp Ser Trp Glu Glu Met Leu Asn Lys Ala Glu Val Gly 275 280 285
His Gly Tyr Met Asp Arg Pro Cys Leu Asn Pro Ala Asp Pro Asp Cys 290 295 300
Pro Ala Thr Ala Pro Asn Lys Asn Ser Thr Lys Pro Leu Asp Met Ala 305 310 315 320
Leu Val Leu Asn Gly Gly Cys His Gly Leu Ser Arg Lys Tyr Met His 325 330 335
Trp Gln Glu Glu Leu Ile Val Gly Gly Thr Val Lys Asn Ser Thr Gly

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345

350

Lys Leu Val Ser Ala His Ala Leu Gln Thr Met Phe Gln Leu Met Thr
355 360 365

Pro Lys Gln Met Tyr Glu His Ph Lys Gly Tyr Glu Tyr Val Ser His
370 375 380

Ile Asn Trp Asn Glu Asp Lys Ala Ala Ala Ile Leu Glu Ala Trp Gln
385 390 395 400

Arg Thr Tyr Val Glu Val Val His Gln Ser Val Ala Gln Asn Ser Thr
405 410 415

Gln Lys Val Leu Ser Phe Thr Thr Thr Thr Leu Asp Asp Ile Leu Lys
420 425 430

Ser Phe Ser Asp Val Ser Val Ile Arg Val Ala Ser Gly Tyr Leu Leu
435 440 445

Met Leu Ala Tyr Ala Cys Leu Thr Met Leu Arg Trp Asp Cys Ser Lys
450 455 460

Ser Gln Gly Ala Val Gly Leu Ala Gly Val Leu Leu Val Ala Leu Ser
465 470 475 480

Val Ala Ala Gly Leu Gly Leu Cys Ser Leu Ile Gly Ile Ser Phe Asn
485 490 495

Ala Ala Thr Thr Gln Val Leu Pro Phe Leu Ala Leu Gly Val Gly Val
500 505 510

Asp Asp Val Phe Leu Leu Ala His Ala Phe Ser Glu Thr Gly Gln Asn
515 520 525

Lys Arg Ile Pro Phe Glu Asp Arg Thr Gly Glu Cys Leu Lys Arg Thr
530 535 540

Gly Ala Ser Val Ala Leu Thr Ser Ile Ser Asn Val Thr Ala Phe Phe
545 550 555 560

Met Ala Ala Leu Ile Pro Ile Pro Ala Leu Arg Ala Phe Ser Leu Gln
565 570 575

Ala Ala Val Val Val Val Phe Asn Phe Ala Met Val Leu Leu Ile Phe
580 585 590

Pro Ala Ile Leu Ser Met Asp Leu Tyr Arg Arg Glu Asp Arg Arg Leu
595 600 605

Asp Ile Phe Cys Cys Phe Thr Ser Pro Cys Val Ser Arg Val Ile Gln
610 615 620

Val Glu Pro Gln Ala Tyr Thr Asp Thr His Asp Asn Thr Arg Tyr Ser
625 630 635 640

Pro Pro Pro Pro Tyr Ser Ser His Ser Phe Ala His Glu Thr Gln Ile
645 650 655

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Thr Met Gln Thr Val Gln Leu Arg Thr Glu Tyr Asp Pro His Thr
665 670

His Val Tyr Tyr Thr Thr Ala Glu Pro Arg Ser Glu Ile Ser Val Gln
675 680 685

Pro Val Thr Val Thr Gln Asp Thr Leu Ser Cys Gln Ser Pro Glu Ser
690 695 700

Thr Ser Ser Thr Arg Asp Leu Leu Ser Gln Phe Ser Asp Ser Ser Leu
705 710 715 720

His Cys Leu Glu Pro Pro Cys Thr Lys Trp Thr Leu Ser Ser Phe Ala
725 730 735

Glu Lys His Tyr Ala Pro Phe Leu Leu Lys Pro Lys Ala Lys Val Val
740 745 750

Val Ile Phe Leu Phe Leu Gly Leu Leu Gly Val Ser Leu Tyr Gly Thr
755 760 765

Thr Arg Val Arg Asp Gly Leu Asp Leu Thr Asp Ile Val Pro Arg Glu
770 775 780

Thr Arg Glu Tyr Asp Phe Ile Ala Ala Gln Phe Lys Tyr Phe Ser Phe
785 790 795 800

Tyr Asn Met Tyr Ile Val Thr Gln Lys Ala Asp Tyr Pro Asn Ile Gln
805 810 815

His Leu Leu Tyr Asp Leu His Arg Ser Phe Ser Asn Val Lys Tyr Val
820 825 830

Met Leu Glu Glu Asn Lys Gln Leu Pro Lys Met Trp Leu His Tyr Phe
835 840 845

Arg Asp Trp Leu Gln Gly Leu Gln Asp Ala Phe Asp Ser Asp Trp Glu
850 855 860

Thr Gly Lys Ile Met Pro Asn Asn Tyr Lys Asn Gly Ser Asp Asp Gly
865 870 875 880

Val Leu Ala Tyr Lys Leu Leu Val Gln Thr Gly Ser Arg Asp Lys Pro
885 890 895

Ile Asp Ile Ser Gln Leu Thr Lys Gln Arg Leu Val Asp Ala Asp Gly
900 905 910

Ile Ile Asn Pro Ser Ala Phe Tyr Ile Tyr Leu Thr Ala Trp Val Ser
915 920 925

Asn Asp Pro Val Ala Tyr Ala Ala Ser Gln Ala Asn Ile Arg Pro His
930 935 940

Arg Pro Glu Trp Val His Asp Lys Ala Asp Tyr Met Pro Glu Thr Arg
945 950 955 960

Leu Arg Ile Pro Ala Ala Glu Pro Ile Glu Tyr Ala Gln Phe Pro Phe

Tyr Leu Asn Gly Leu Arg Asp Thr Ser Asp Phe Val Glu Ala Ile Glu
980 985 990

Lys Val Arg Thr Ile Cys Ser Asn Tyr Thr Ser Leu Gly Leu Ser Ser
995 1000 1005

Tyr Pro Asn Gly Tyr Pro Phe Leu Phe Trp Glu Gln Tyr Ile Gly Leu
1010 1015 1020

Arg His Trp Leu Leu Leu Phe Ile Ser Val Val Leu Ala Cys Thr Phe
1025 1030 1035 1040

Leu Val Cys Ala Val Phe Leu Leu Asn Pro Trp Thr Ala Gly Ile Ile
1045 1050 1055

Val Met Val Leu Ala Leu Met Thr Val Glu Leu Phe Gly Met Met Gly
1060 1065 1070

Leu Ile Gly Ile Lys Leu Ser Ala Val Pro Val Val Ile Leu Ile Ala
1075 1080 1085

Ser Val Gly Ile Gly Val Glu Phe Thr Val His Val Ala Leu Ala Phe
1090 1095 1100

Leu Thr Ala Ile Gly Asp Lys Asn Arg Arg Ala Val Leu Ala Leu Glu
1105 1110 1115 1120

His Met Phe Ala Pro Val Leu Asp Gly Ala Val Ser Thr Leu Leu Gly
1125 1130 1135

Val Leu Met Leu Ala Gly Ser Glu Phe Asp Phe Ile Val Arg Tyr Phe
1140 1145 1150

Phe Ala Val Leu Ala Ile Leu Thr Ile Leu Gly Val Leu Asn Gly Leu
1155 1160 1165

Val Leu Leu Pro Val Leu Leu Ser Phe Phe Gly Pro Tyr Pro Glu Val
1170 1175 1180

Ser Pro Ala Asn Gly Leu Asn Arg Leu Pro Thr Pro Ser Pro Glu Pro
1185 1190 1195 1200

Pro Pro Ser Val Val Arg Phe Ala Met Pro Pro Gly His Thr His Ser
1205 1210 1215

Gly Ser Asp Ser Ser Asp Ser Glu Tyr Ser Ser Gln Thr Thr Val Ser
1220 1225 1230

Gly Leu Ser Glu Glu Leu Arg His Tyr Glu Ala Gln Gln Gly Ala Gly
1235 1240 1245

Gly Pro Ala His Gln Val Ile Val Glu Ala Thr Glu Asn Pro Val Phe
1250 1255 1260

Ala His Ser Thr Val Val His Pro Glu Ser Arg His His Pro Pro Ser
1265 1270 1275 1280

Asn Pro Arg Gln Pro His Leu Asp Ser Gly Ser Leu Pro Pro Gly
1285 1290 1295

Arg Gln Gly Gln Gln Pro Arg Arg Asp Pro Pro Arg Glu Gly Leu Trp
1300 1305 1310

Pr Pro Leu Tyr Arg Pro Arg Arg Asp Ala Phe Glu Ile Ser Thr Glu
1315 1320 1325

Gly His Ser Gly Pro Ser Asn Arg Ala Arg Trp Gly Pro Arg Gly Ala
1330 1335 1340

Arg Ser His Asn Pro Arg Asn Pro Ala Ser Thr Ala Met Gly Ser Ser
1345 1350 1355 1360

Val Pro Gly Tyr Cys Gln Pro Ile Thr Thr Val Thr Ala Ser Ala Ser
1365 1370 1375

Val Thr Val Ala Val His Pro Pro Pro Val Pro Gly Pro Gly Arg Asn
1380 1385 1390

Pro Arg Gly Gly Leu Cys Pro Gly Tyr Pro Glu Thr Asp His Gly Leu
1395 1400 1405

Phe Glu Asp Pro His Val Pro Phe His Val Arg Cys Glu Arg Arg Asp
1410 1415 1420

Ser Lys Val Glu Val Ile Glu Leu Gln Asp Val Glu Cys Glu Glu Arg
1425 1430 1435 1440

Pro Arg Gly Ser Ser Ser Asn
1445

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